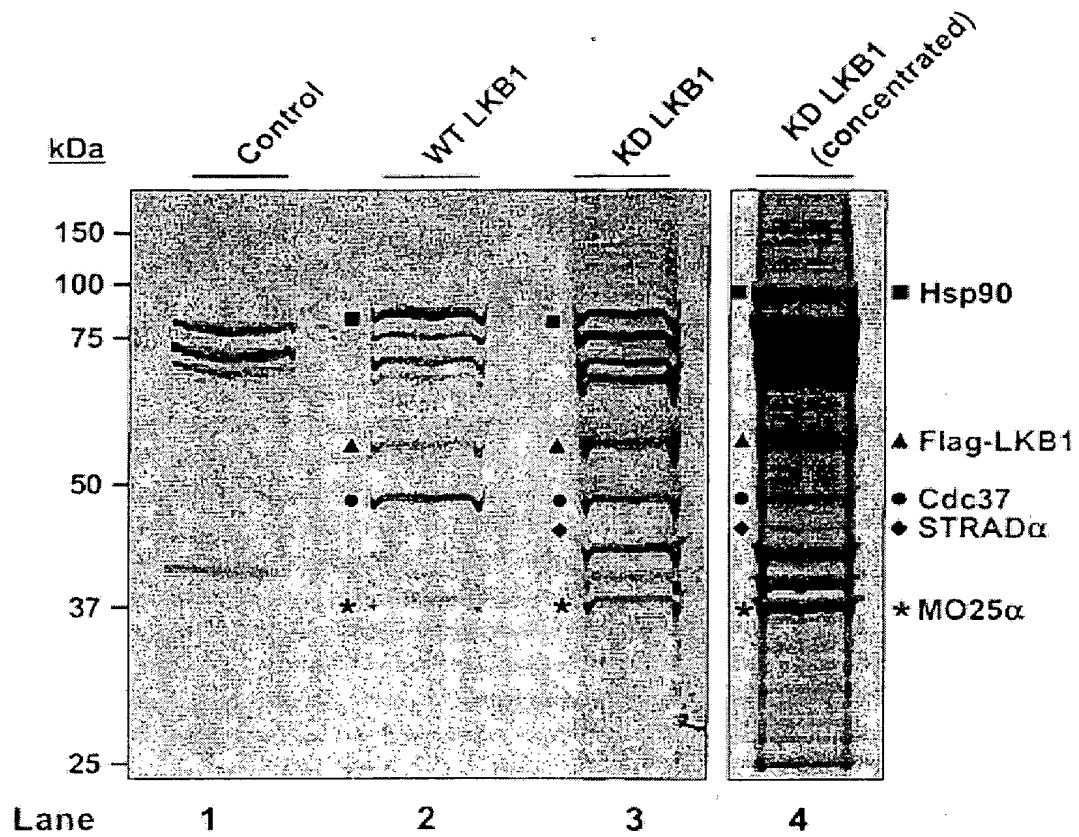
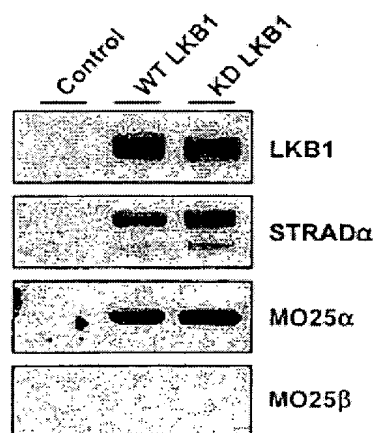


Figure 1A



**Figure 1B**

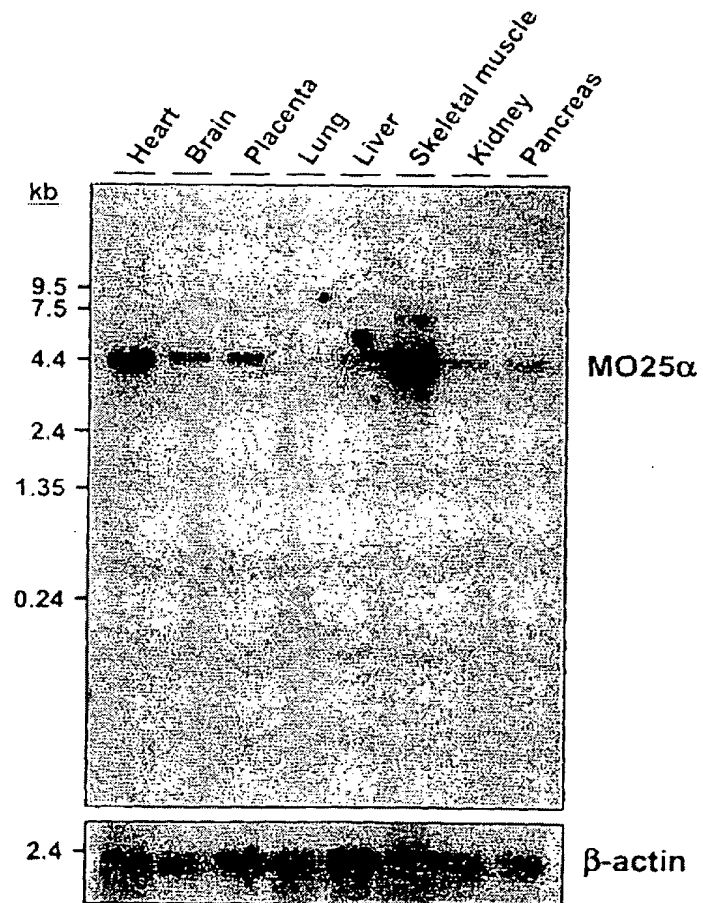
	Protein name	Peptide matches	% sequence coverage	NCBI gi number
■	Hsp90	15/44	30%	20149594
▲	Flag-LKB1	14/46	35%	7106425
●	Cdc37	31/72	59%	5901922
◆	STRAD $\alpha$	11/80	34%	12060855
*	MO25 $\alpha$	17/37	47%	7706481

**Figure 1C**

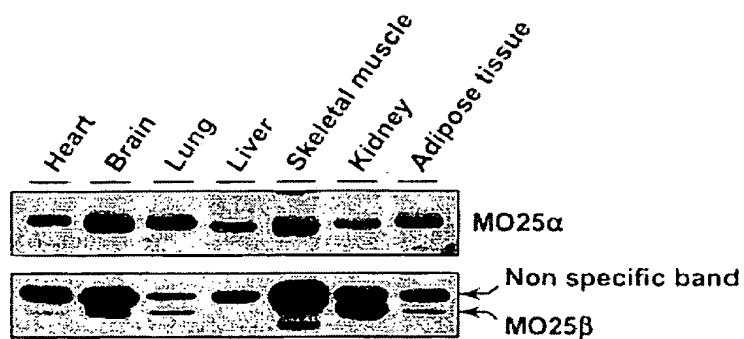
## Figure 2A

(SEQ ID NO:11) hMO25 $\alpha$	1	MPL- <del>PF</del> GKSHKSPAD <del>V</del> VKNLKES <del>A</del> ILEKQD-----ISDKKAEKATEEVSKNLVA
(SEQ ID NO:12) hMO25 $\beta$	1	MPL--FSKSHKNPAE <del>V</del> VTKENLAILEKQ-----DKKTEKASEEVSKSLQA
(SEQ ID NO:15) dMO25	1	MPL--FGKSKSEV <del>E</del> VKSLKEA <del>I</del> NALEAG-----DKKVEKACEEVSKNLVS
(SEQ ID NO:13) cMO25 $\alpha$	1	MLKPLFGK <del>E</del> DKPAD <del>V</del> VKNL <del>E</del> AL <del>L</del> VA <del>T</del> GHG-----TNTSEKVEKAI <del>E</del> ET <del>E</del> KMLAL
(SEQ ID NO:14) cMO25 $\beta$	1	MEL-LFGKSHKSPAD <del>V</del> VKT <del>L</del> EVLT <del>L</del> ILAKLP <del>P</del> PKLDK <del>D</del> GNICSDK <del>K</del> Y <del>E</del> KAL <del>E</del> EVSK <del>N</del> LVA
(SEQ ID NO:11) hMO25 $\alpha$	50	MKE <del>L</del> LYG <del>H</del> --NEKEP-QTEAVAQAQELYN <del>S</del> GLPSTL <del>A</del> ADIQLIDFEGKKDVAQIFNN <del>L</del>
(SEQ ID NO:12) hMO25 $\beta$	46	MKE <del>L</del> LYG <del>H</del> --NEKEP-PT <del>E</del> AVAQAQELYS <del>S</del> GLLVTL <del>A</del> ADIQLIDFEGKKDVTQIFNN <del>L</del>
(SEQ ID NO:15) dMO25	46	MKN <del>L</del> LYG <del>S</del> --SEAEPPADYVVAQAQELYN <del>S</del> NLL <del>L</del> ILIONL <del>H</del> IDFEGKKHVALIFNN <del>L</del>
(SEQ ID NO:13) cMO25 $\alpha$	53	AKTFYGE <del>D</del> ANEPNN---E <del>O</del> VT <del>L</del> AQ <del>E</del> VA <del>N</del> FM <del>L</del> PLIK <del>L</del> HL <del>H</del> EPFECKKDVASEFAN <del>L</del>
(SEQ ID NO:14) cMO25 $\beta$	60	IKSFY <del>G</del> ND <del>S</del> AE <del>P</del> SPSEHV <del>V</del> QVAQAQELYN <del>S</del> NLL <del>L</del> PLIK <del>L</del> ML <del>P</del> K <del>P</del> FEFECKKDV <del>E</del> QIFNN <del>L</del>
(SEQ ID NO:11) hMO25 $\alpha$	107	RRQIGTRSP <del>T</del> VEYICTOONILE <del>M</del> LLKGYE--SP <del>E</del> IALNCG <del>M</del> MLRECIRHEPLAKIIL <del>S</del>
(SEQ ID NO:12) hMO25 $\beta$	103	RRQIGTRSP <del>T</del> VEYIS <del>A</del> PHILE <del>M</del> LLKGYE--AP <del>O</del> I <del>A</del> LR <del>C</del> G <del>M</del> MLRECIRHEPLAKIIL <del>S</del>
(SEQ ID NO:15) dMO25	104	RRQIGTRSP <del>T</del> VEYICT <del>P</del> ELL <del>E</del> TL <del>L</del> AGYEDAH <del>P</del> IALNSG <del>T</del> MLRECARYEALAKIIL <del>S</del>
(SEQ ID NO:13) cMO25 $\alpha$	110	RRQIGTRSP <del>T</del> VEYIA <del>A</del> SP <del>E</del> ILL <del>L</del> TL <del>L</del> GYE--OP <del>EIALTCG<del>S</del>MLRE<del>A</del>IRHEHLAKIIL<del>S</del></del>
(SEQ ID NO:14) cMO25 $\beta$	120	RRQIGTRSP <del>T</del> VEYI <del>G</del> ARPEILL <del>L</del> Q <del>L</del> OSYS--VP <del>EIAL<del>C</del>CG<del>M</del>MLRESIR<del>H</del>HLAKIIL<del>S</del></del>
(SEQ ID NO:11) hMO25 $\alpha$	165	Q <del>R</del> Y <del>D</del> FF <del>E</del> V <del>V</del> ESTFDIASDAF <del>T</del> FKOLLTRH <del>K</del> ILSAEFL <del>E</del> CH <del>V</del> DEFF--SEVENILL <del>S</del> SENV
(SEQ ID NO:12) hMO25 $\beta$	161	Q <del>R</del> Y <del>D</del> FF <del>E</del> V <del>V</del> ESTFDIASDAF <del>T</del> FKOLLTRH <del>K</del> ILVA <del>F</del> FL <del>E</del> CH <del>V</del> DEFF--EDYENILL <del>S</del> SENV
(SEQ ID NO:15) dMO25	164	E <del>P</del> SKFF <del>E</del> V <del>V</del> ESTFDIASDAF <del>T</del> FKOLLTRH <del>K</del> ILCAEFL <del>D</del> AN <del>V</del> DEFF--SQHYOILL <del>S</del> SENV
(SEQ ID NO:13) cMO25 $\alpha$	168	Y <del>F</del> Q <del>R</del> FF <del>E</del> V <del>V</del> ESDV <del>F</del> DIADAFST <del>F</del> FKOLL <del>T</del> TH <del>K</del> ILCAEFL <del>D</del> AN <del>V</del> DEFF--GOVSALT <del>S</del> SENV
(SEQ ID NO:14) cMO25 $\beta$	178	V <del>E</del> FTFF <del>L</del> V <del>V</del> SEV <del>F</del> DI <del>S</del> DAFST <del>F</del> FKOLL <del>T</del> TH <del>K</del> ILIAEFL <del>D</del> SN <del>VDTFF--AQVONILL<del>S</del>SENV</del>
(SEQ ID NO:11) hMO25 $\alpha$	224	V <del>T</del> TRQSLKLLGELLDRHNF <del>E</del> MTKYISK <del>P</del> ENLKLMMNLLRD <del>K</del> SRNIOFEAFHVFKVFVA
(SEQ ID NO:12) hMO25 $\beta$	220	V <del>T</del> TRQSLKLLGELLDRHNF <del>E</del> MTKYISK <del>P</del> ENLKLMMNLLRD <del>K</del> SE <del>N</del> IOFEAFHVFKVFVA
(SEQ ID NO:15) dMO25	224	V <del>T</del> TRQSLKLLGELLDRHNF <del>E</del> MT <del>E</del> YISEPENLKLMMN <del>L</del> LK <del>S</del> SRNIOFEAFHVFKVFVA
(SEQ ID NO:13) cMO25 $\alpha$	227	V <del>T</del> TRQSLKLLGELLDRHNF <del>E</del> MTKYI <del>S</del> SPENL <del>K</del> LM <del>L</del> ELLRD <del>K</del> SRNIOFEAFHVFKVFVA
(SEQ ID NO:14) cMO25 $\beta$	237	V <del>T</del> TRQSLKLLGELLDRHNF <del>E</del> MTKYIS <del>N</del> PENL <del>K</del> LM <del>L</del> ELLRD <del>K</del> SRNIOFEAFHVFKVFVA
(SEQ ID NO:11) hMO25 $\alpha$	284	NP <del>N</del> K <del>T</del> Q <del>P</del> IL <del>L</del> DILL <del>N</del> CAKLEFL <del>S</del> SG <del>F</del> NDRT <del>E</del> DEQFNDEK <del>T</del> YLKQ <del>I</del> ELKRP <del>A</del> QOE <del>A</del> --
(SEQ ID NO:12) hMO25 $\beta$	280	SP <del>H</del> K <del>T</del> Q <del>P</del> IL <del>L</del> DILL <del>N</del> QPKLEFL <del>S</del> SG <del>F</del> OKERT <del>E</del> DEQFAD <del>E</del> KAYLIKQ <del>I</del> ELK <del>T</del> AP----
(SEQ ID NO:15) dMO25	284	NP <del>N</del> K <del>P</del> PI <del>L</del> DILL <del>R</del> NO <del>T</del> KL <del>V</del> FL <del>E</del> N <del>F</del> HTD <del>R</del> E <del>E</del> DEQFNDEKAYLIKQ <del>I</del> ELK <del>P</del> LEA----
(SEQ ID NO:13) cMO25 $\alpha$	287	NP <del>N</del> K <del>P</del> PI <del>L</del> DILL <del>R</del> NR <del>D</del> KL <del>V</del> FL <del>E</del> AFH <del>N</del> DR <del>T</del> NOEQFNDEKAYLIKQ <del>I</del> EL <del>E</del> V----
(SEQ ID NO:14) cMO25 $\beta$	297	NP <del>N</del> K <del>P</del> PI <del>S</del> DILL <del>R</del> NR <del>E</del> KL <del>V</del> FL <del>E</del> SG <del>F</del> HNDRT <del>E</del> DEQFNDEKAYLIKQ <del>I</del> OE <del>M</del> KSS <del>P</del> KEAK <del>K</del> P
(SEQ ID NO:11) hMO25 $\alpha$		-----
(SEQ ID NO:12) hMO25 $\beta$		-----
(SEQ ID NO:15) dMO25		-----
(SEQ ID NO:13) cMO25 $\alpha$		-----
(SEQ ID NO:14) cMO25 $\beta$	357	KSKEDENQEPAGPSEGPSTSQ

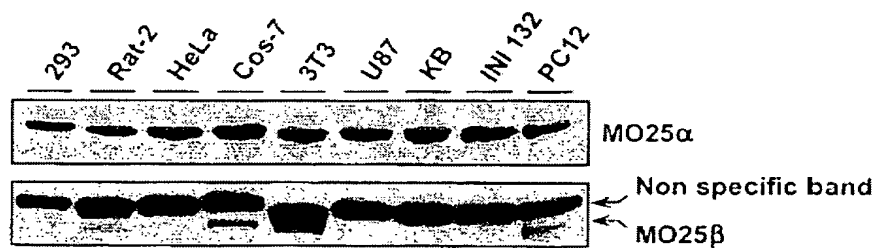
**Figure 2B**



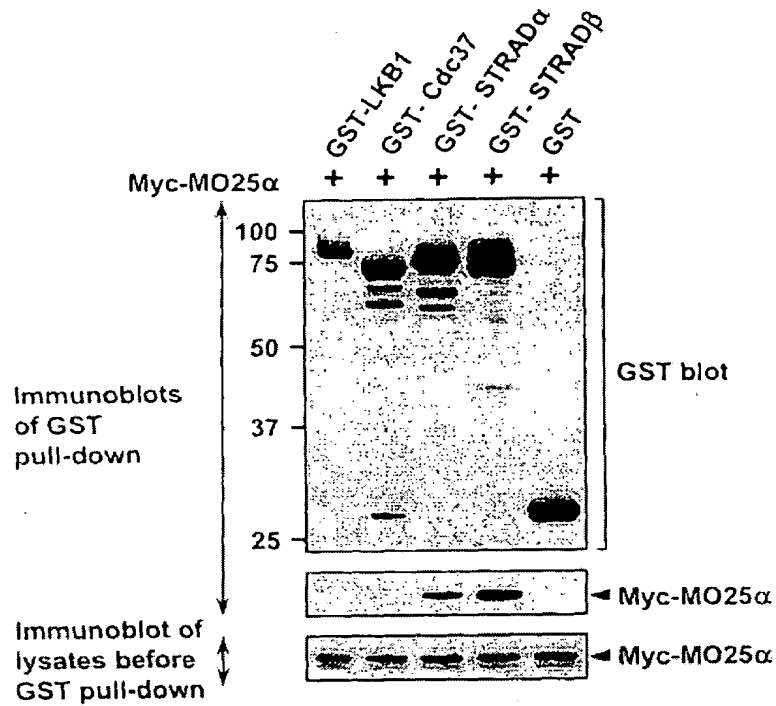
**Figure 2C**



**Figure 2D**



**Figure 4A**



**Figure 4B**

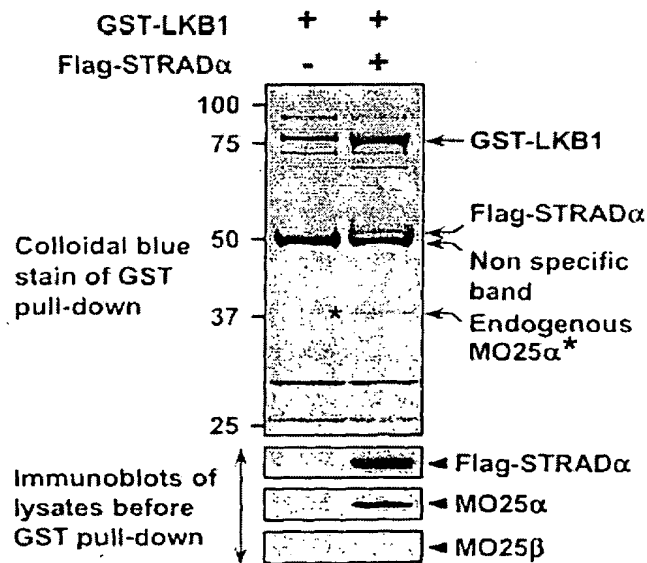
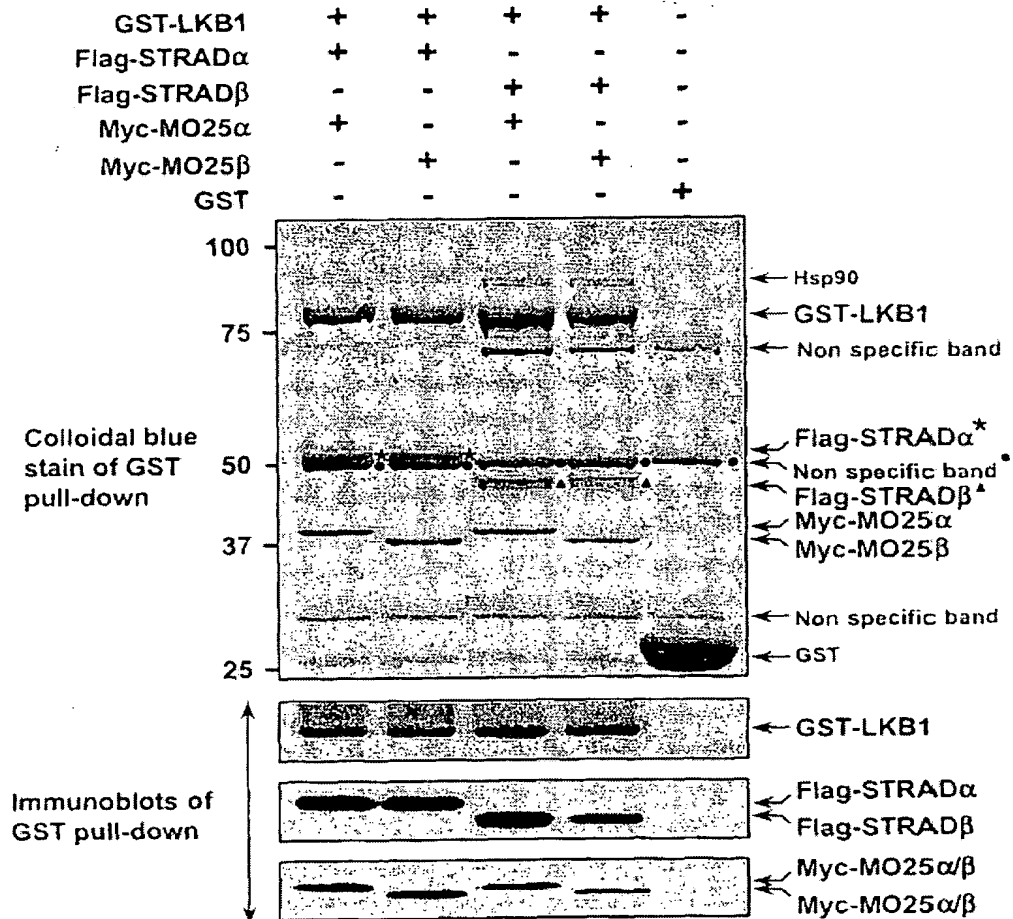


Figure 4C



**Figure 5 (continued)**

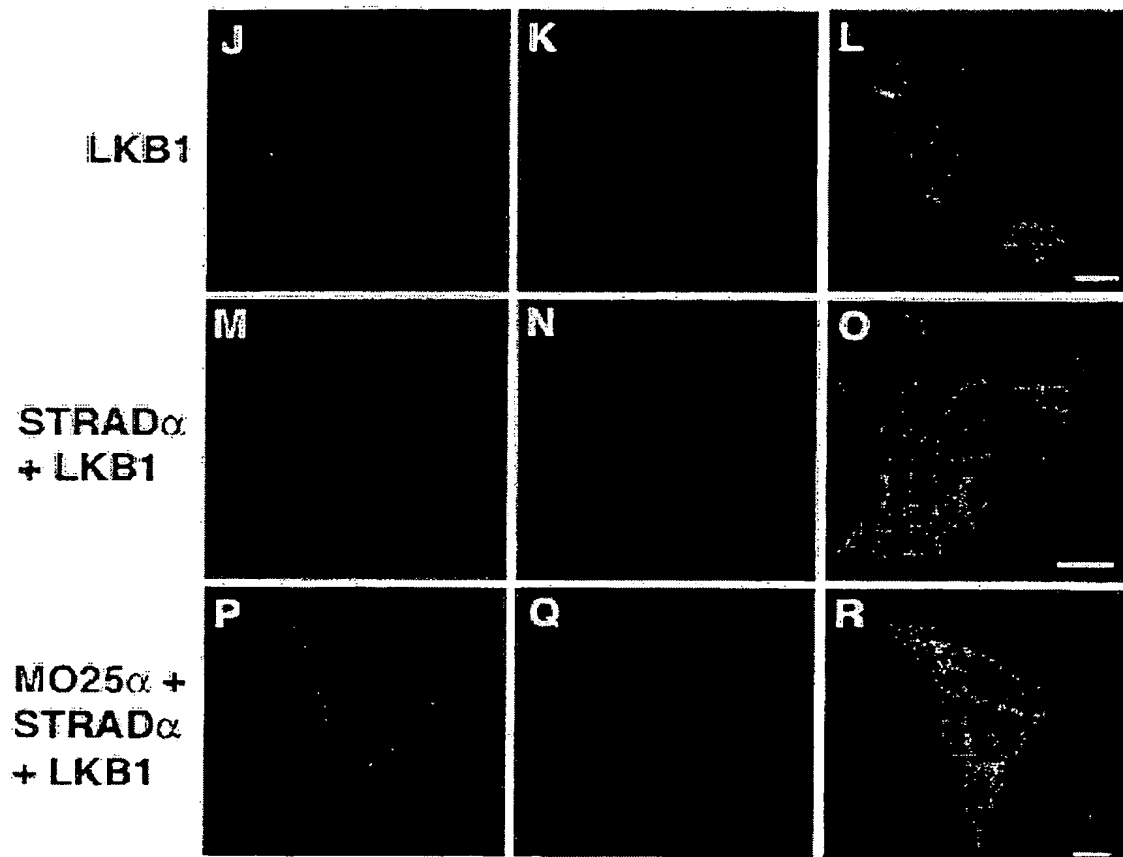




Figure 6A

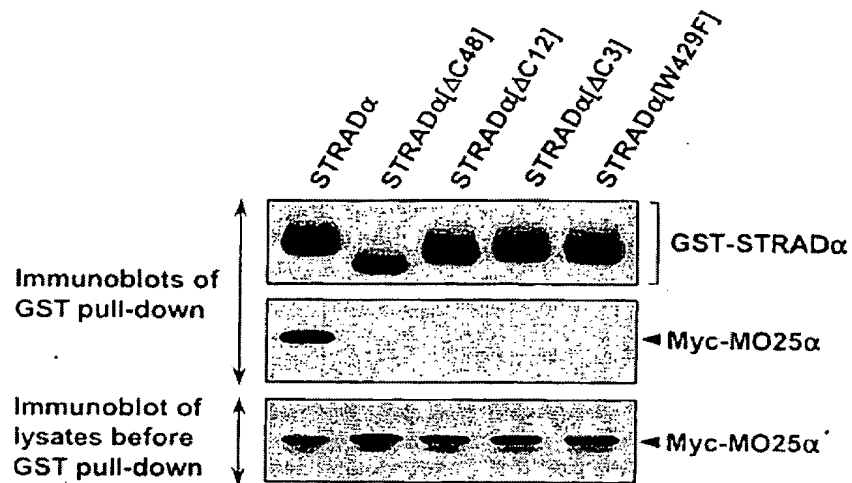
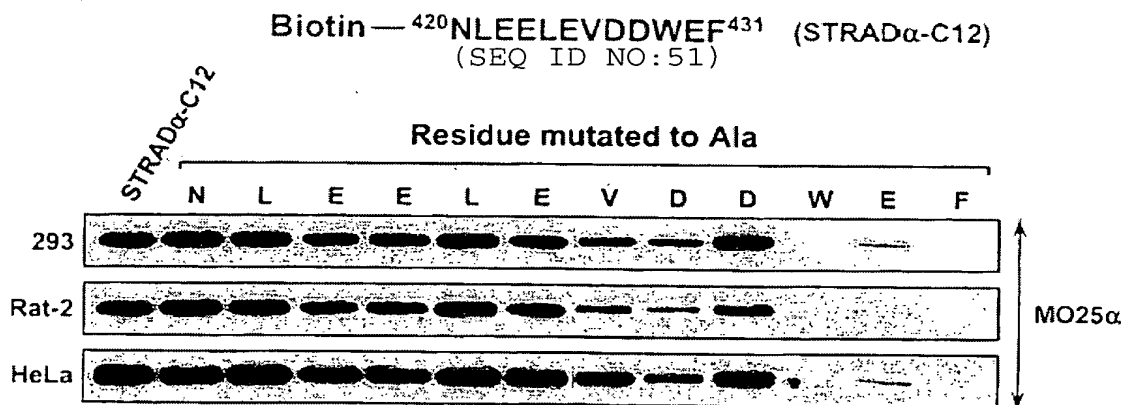
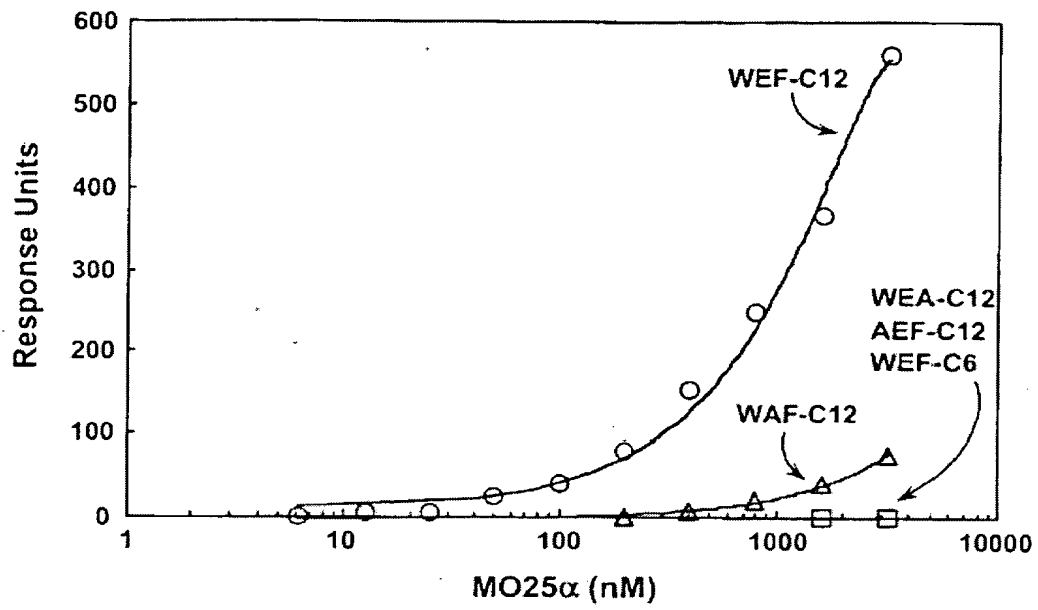


Figure 6B



**Figure 6C**

(SEQ ID NO:9)	hSTRAD $\alpha$	1	MSFLVSKPERARRRVSEKFIIVEGLRDLLELFGBOPPGDTIRKTNDAASSEIASFSKQEVMS
(SEQ ID NO:10)	hSTRAD $\beta$	1	-----MSLIDDOCTSSITQVBSLRPEK-----QSETSIQOYLVDPEPLSWSRPSTRASEV
(SEQ ID NO:56)	hSPAK	1	----MAEPGSGPVHVQLPQCAAPYTAAAAAAPAAATAAPAPAAPAPAPAPAPAPAPAPAPAPAP
(SEQ ID NO:57)	hOSR1	1	-----MSEDSSAE
(SEQ ID NO:9)	hSTRAD $\alpha$	61	SFLPEGGCYELLTVIGKGFEDLMTVILARYKPTGEYVTMRINLEACSNEWVTFLQGEYH
(SEQ ID NO:10)	hSTRAD $\beta$	50	LCSTNVSHVELQVEIGRGFENLTSVHLARHTPTGTILTITKTNLENCNEERLKAQKAVI
(SEQ ID NO:56)	hSPAK	57	GWPIICRDAYELQEVIGSG--ATAVVOAALCKPRQERVAIKRINLEKCQOTSMDELLK-EIQ
(SEQ ID NO:57)	hOSR1	9	PWSINRDDYELQEVIGSG--ATAVVOAAYCAKKEKVAIKRINLEKCQOTSMDELLK-EIQ
(SEQ ID NO:9)	hSTRAD $\alpha$	121	VSKLFNHPNIVPYRAITFADNELWVTSFAYGSAKDELICTHFMDG-----FNELATAY
(SEQ ID NO:10)	hSTRAD $\beta$	110	LSHFFHHPNITTYITVETVGSWLWISPPAYGSASQDSTYFPEG-----MSEHDIRN
(SEQ ID NO:56)	hSPAK	114	AMSQCSPHNVITYYTSFVVKDELWVMKLSGGSMLEIKYIVNRGEHKNGVDEBATIAT
(SEQ ID NO:57)	hOSR1	66	AMSQCSPHNVITYYTSFVVKDELWVMKLSGGSVLDIKHIVAKGEHKSQVDEBATIAT
(SEQ ID NO:9)	hSTRAD $\alpha$	175	ILQGLKALDYTHMGYVHRSVKASHILLSVDCKVYISGLRSNLSIISHGORQRRVHDFP
(SEQ ID NO:10)	hSTRAD $\beta$	164	ILFGAMRGLNYLHONGCIHRSVKASHILLSGDGLVTSGLSHLHSLVKHGQRHRAVYDFP
(SEQ ID NO:56)	hSPAK	174	ILKEVLEGLDYLHNGQIHRDEKAGNILEGEDGSVQIDFGVSAFLATGGDVTR--NKVR
(SEQ ID NO:57)	hOSR1	126	ILKEVLEGLDYLHNGQIHRDVKAGNILEGEDGSVQIDFGVSAFLATGGDITR--NKVR
(SEQ ID NO:9)	hSTRAD $\alpha$	235	KYSVKVLPWTSPEVERQNGGYDAKSDIISVGITACELANGHVPKIDMPATOMLDEKILG
(SEQ ID NO:10)	hSTRAD $\beta$	224	QFSTSVQPVTSPELRODHGYNVKSDIISVGITACELASGVPEQDMHRTOMLDEKILG
(SEQ ID NO:56)	hSPAK	232	KTFVGTTCWMAPEVMECVRGYDFKADINSFGITATELATGAAPHHKYPPMKYLLITLON
(SEQ ID NO:57)	hOSR1	184	KTFVGTTCWMAPEVMECVRGYDFKADINSFGITATELATGAAPHHKYPPMKYLLITLON
(SEQ ID NO:9)	hSTRAD $\alpha$	295	---TTP-----CLL-DTSTIPAEELTSPSRSVANSGL-SDSL
(SEQ ID NO:10)	hSTRAD $\beta$	284	-PPYSP-----LL-DISIFPQESRMKNSQSGVDSGIGESYL
(SEQ ID NO:56)	hSPAK	291	DPPTLETGVDEKEMKKYKGKSRKSLCLQKDPSKRPTAAELKCKFFQKAKNR-EYLT
(SEQ ID NO:57)	hOSR1	243	DPPTLETGVDEKEMKKYKGKSRKSLCLQKDPEKRPTAAELKCKFFQKAKNK-SGLQ
(SEQ ID NO:9)	hSTRAD $\alpha$	328	TTSTPRPSNGDWPSHPYHRT--FSPFHFFVFEQCLQRNPDARPSASTLLNHSFKQIKRR
(SEQ ID NO:10)	hSTRAD $\beta$	318	VSSGTHTVNSDRLHTPSSKT--FSPAFFSLVQLCLQQDPKRPASALLSHVFFKMKEE
(SEQ ID NO:56)	hSPAK	350	EKLLTRTPBIAQRAKKVRRVPGSSGHLKHTEDGDWESDDDEDEKSEEGKAASQEKSR
(SEQ ID NO:57)	hOSR1	302	EKLLQRAPTISERAKKVRRVPGSSGHLKHTEDGGWESDDDEDESEEGKAASISQLRSP
(SEQ ID NO:9)	hSTRAD $\alpha$	386	ASK-----ALPELFRP-----VTPITNE
(SEQ ID NO:10)	hSTRAD $\beta$	376	SQD-----SILSLFP-----PAY
(SEQ ID NO:56)	hSPAK	410	VKE--ENPEITAVSAS-----ILPEQHS-----ESVHDSQGPANEDY
(SEQ ID NO:57)	hOSR1	362	VKESISNSSEFPITDTPVGTLLQVPEISAHLPQAPAGQIATOPTQTSPPITAEPAKTAQAL
(SEQ ID NO:9)	hSTRAD $\alpha$	404	EGSQ-S---QDHSCTFGLVTNLEELVDDREF-----
(SEQ ID NO:10)	hSTRAD $\beta$	389	NKPSIS--LPPVLPTWTEPCDFPDEKDSYAEF-----
(SEQ ID NO:56)	hSPAK	447	REAS-S---CAVNLVLRLRNSKELNDIRFEFTPGRDTAIGVSQELFSAGLVDGDDVI
(SEQ ID NO:57)	hOSR1	422	SSCGSGSQETKIPHSVLVLRLRNSKELNDIRFEFTPGRDTAIGVSQELFSAGLVDGDDVI
(SEQ ID NO:9)	hSTRAD $\alpha$	.	-----
(SEQ ID NO:10)	hSTRAD $\beta$	.	-----
(SEQ ID NO:56)	hSPAK	502	VAANLOKIVDEPKALKLITFKLASGCGSGHIPDEVKLIGFAQLSIS
(SEQ ID NO:57)	hOSR1	482	VAANLOKIVDEPKSNKLVITFKLASGCGSGHIPDEVKLIGFAQLSIS

Figure 12

```

(SEQ ID NO:58) Tos3      11  ..LPRSSLLYNNASNSSSRRIKETRKVKLLYNPLTKR.....Q...ILNNFEILATLGNQG
(SEQ ID NO:59) Pak1      94  ..TPTTTSSFCSSGSSKNKVEETNRISLTYDPVSKR.....K...VLNTYEIIKELGHGQ
(SEQ ID NO:61) CamKKβ    121 CICIPSLPYSPVSSPQSSPRLPRRPTVESHVHSITGM.....QDCVQLNQYTLKDEIGKGS
(SEQ ID NO:6)  LKB1       7   QQLGMFTGELMSVGMDFIHRIDSTEVIYOP..RR.....KRAKLIQKYLMDLLGEGS
(SEQ ID NO:60) Elm1      39  TSSFGSSFSQOKPTYSTIIGENIHTILDEIRPYVKKITVSDQDKKTINQYTLGVSAGSQ
(SEQ ID NO:62) consensus 121  p s s s s s rik tv l y pltkr q ilnny i lg Gq

(SEQ ID NO:58) Tos3      61  YGKVKLARDLGTGALVAIKILNRFEKRS....GYSL.....QLKV.EN.....
(SEQ ID NO:59) Pak1     144  HGKVKLARDILSKQLVAIKIVDRHEKKQRKFFTFIK.....SSKISEN.....
(SEQ ID NO:61) CamKKβ    176  YGVVKLAYNENDNTYYAMKVLK..KKLIRQAGFPR.....RPPPRGTRPAPGGCQIP
(SEQ ID NO:6)  LKB1      60  YGKVKELVDSETLCRRRAVKILK..KKLRR.....
(SEQ ID NO:60) Elm1     99  FGYVRKAYSSTLGKVVAVKIIIPKPEWNAQQYQSVNQVMRQIQWLWKSQKITTNSGNEAMR
(SEQ ID NO:62) consensus 181  yGkVkla d t lvaikil k kk k y k

(SEQ ID NO:58) Tos3      99  ....PRVNOEIEVMKRCHHE.NVVELYEILNDPESTKVYLVLEYCSRGPVKWCPCENKMEI
(SEQ ID NO:59) Pak1     187  ....DKIKREIAIMKKCHHK.HVVQLIEVLDDLSRKIYLVLEYCSRGEVVKWCPDCMES
(SEQ ID NO:61) CamKKβ    227  RGPTEQVYQEIAILKKLDHP.NVVKLVEVLDDPNEDHLYMVFEVLNQGPV.....MEV
(SEQ ID NO:6)  LKB1      89  PNGEANVKKEIQLLRLRHK.NVIQLVDVLYNEEKQKMYMVEYC.....VCGMQEM.L
(SEQ ID NO:60) Elm1     159  LMNIEKCRWEIFAASRLRNNVHIVRLIECLDSPFSESIWIVTNWCSLGELQWKRDDDEDI
(SEQ ID NO:62) consensus 241  drvk EI vmkrlhh nvv LlievLddp s kvylVleycs g v wc mei

(SEQ ID NO:58) Tos3     154  .KAVGPSILTFQO...SRKVVLDDVSGLEYLHSGGITHRDIKPSNLLISSNGTV.KISD
(SEQ ID NO:59) Pak1     242  .DAKGPSLLSFQE....TREILRGVVLGLEYLHYOGIIHRDIKPANLLISGDGTV.KISD
(SEQ ID NO:61) CamKKβ    279  .PTLKE..LSEDO...ARFYFQDLIKGIEYLHYQKIIHRDIKPSNLLVGEDGHI.KIAD
(SEQ ID NO:6)  LKB1     141  .DSVPEKRFPVCQ...ANGYFCQLIDGLEYLHSGGIVHKDIKPGNLLLTGGTL.KISD
(SEQ ID NO:60) Elm1     219  LPQWKKIVISNCSVSTFAKKILEDMTKGLEYLHSGGCIHRDIKPSNILLDEEEKVAKLSD
(SEQ ID NO:62) consensus 301  v p ils q ar vv dvv GLEYLHsQgiiHrDIKPSnllis dgtv KisD

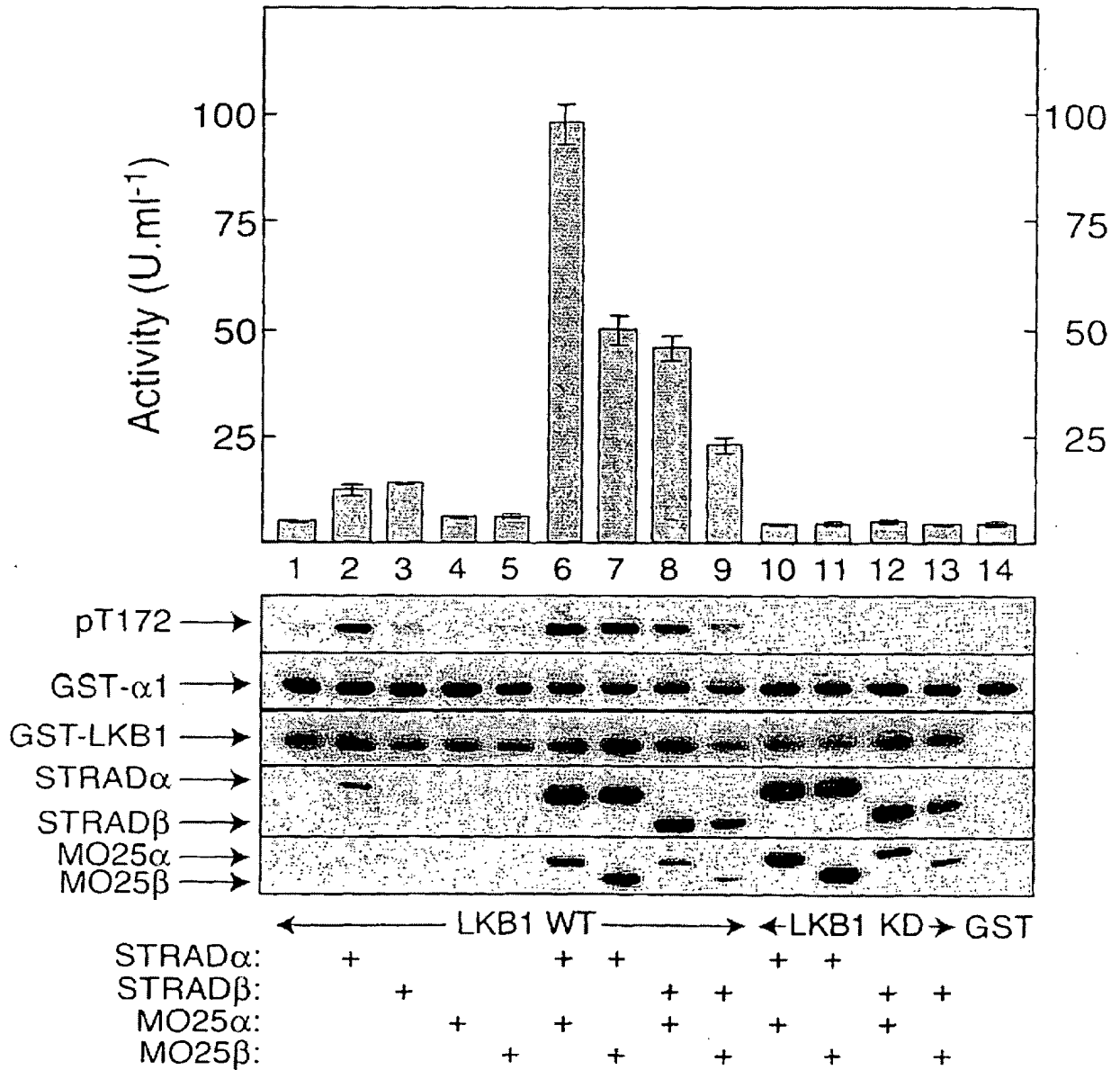
(SEQ ID NO:58) Tos3     208  FG..VAM.STATGSTNIQSSHEQLLKSRA LGTPAFFAPELCSTEKEY.....
(SEQ ID NO:59) Pak1     296  FG..VSLAASSTNSSDSSESLELELAKTVGTPAFFAPEMCLGEDAFTRYNLTKENLFRG
(SEQ ID NO:61) CamKKβ    331  FG..V.....SNEFKGS..DALLSNTVGTPAFMAPESLS.....ETRKIFSG
(SEQ ID NO:6)  LKB1     195  LG..VAEALHPFAADDTCTRSQ.....GSPAQFPPEIANGLDTF.....
(SEQ ID NO:60) Elm1     279  FGSCIFTPQSLPFSDFANFEDCFQRELNKIVGTAFIAPELCHLGNSKRDFVTD.....
(SEQ ID NO:62) consensus 361  fG v t s d s l r vGtPAF aPElc y

(SEQ ID NO:58) Tos3     252  SC.SSAIDIWSLGVTIYCLLFGKLPFNANSGLLEFDSIINKPLEFPSYEEMLNATSGIT
(SEQ ID NO:59) Pak1     354  SCISFMIDIWAVGVTLYCLLFGMLPFFSDFELKLFKEKIVNDPLKFPTFKEIQSNKVSQVS
(SEQ ID NO:61) CamKKβ    369  K....ALDVWAMGVTLYCFVFGQCPFMDERIMCLHSHKIKSQALEFPDQPDIA.....
(SEQ ID NO:6)  LKB1     233  ...GFKVDIWSAGVTLYNITTGLYPFEGDNIYKLFENIGKGSYAIP.....
(SEQ ID NO:60) Elm1     332  ...GFKLDIWSLGVTIYCLLYNELPFFGENEFETYHKIIEVSLSSKINGNTLNDLVIKRL
(SEQ ID NO:62) consensus 421  f iDiWslGVTLlycllfg lPf ad l lfdkIi l fp em

(SEQ ID NO:58) Tos3     311  M.EEYT...DAKDLLKKLLQKDPDKRIKLADIKVHPFMC....HYGKSDAASVL...TN
(SEQ ID NO:59) Pak1     414  CEEYE...MAKDLLKKLLEKNPQKRMTIPAIIKHFFVS.WDFDHVPENDEKLLS...SV
(SEQ ID NO:61) CamKKβ    417  ....E...DLKDITRMLDKNPESRIVVPEIKLHPWVTRHGAEPLPSEDENCTLVEVTE
(SEQ ID NO:6)  LKB1     276  .GDCGP...PLSLLKGMLEYEPAKRFSIRQIROHSWFRK...KHPPAEAPVPIPPSPDT
(SEQ ID NO:60) Elm1     389  LEKDVTLRISIQDLVKVLSRDQPIDSRNHSQISSSS.VNPVRNEGVPVRRFFGRLLTKKKG
(SEQ ID NO:62) consensus 481  ee lkDliklleknP kri l Ik hpfv dh p d vl t

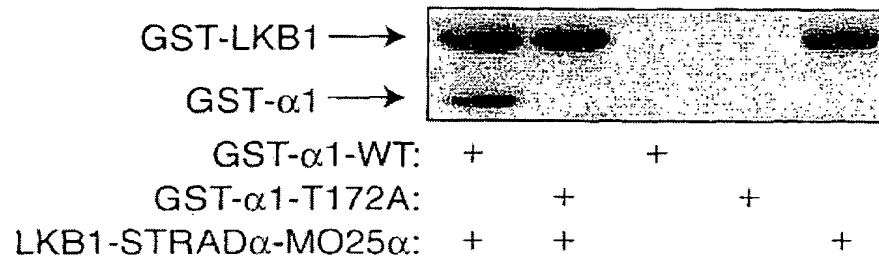
(SEQ ID NO:58) Tos3     359  LETFHELKVSP.....SSCKRVELVSLPVNSSFASLDSVYMFNDHNNLRTGADRNS
(SEQ ID NO:59) Pak1     467  LE..QKLRF.....QCNQTDQFE.PISISKHELKNAV.....SGVGKKIKESV
(SEQ ID NO:61) CamKKβ    469  EEVENSVKHIPSLATVILVKTMIKRSPGNPFEGSRREERSLSAPGNLLTKQGSEDNLQK
(SEQ ID NO:6)  LKB1     329  KDRWRSMTVVYPYLEDLHGADEDEDLFDIEDDIYTDQFTVPGQVPEEEASHNGQRRGLPK
(SEQ ID NO:60) Elm1     448  KKTSGKGDKVLVSATSKVTPSIHIDEEDPKECFSTTVLRSSPDSSDYCSSLGEAEIQVT
(SEQ ID NO:62) consensus 541  e lk p l rve pv s lks s lg

```

**Figure 15A**Activation of AMPK $\alpha$ 1 catalytic domain by LKB1

**Figure 15B**

Phosphorylation of AMPK $\alpha$ 1 catalytic domain by LKB1



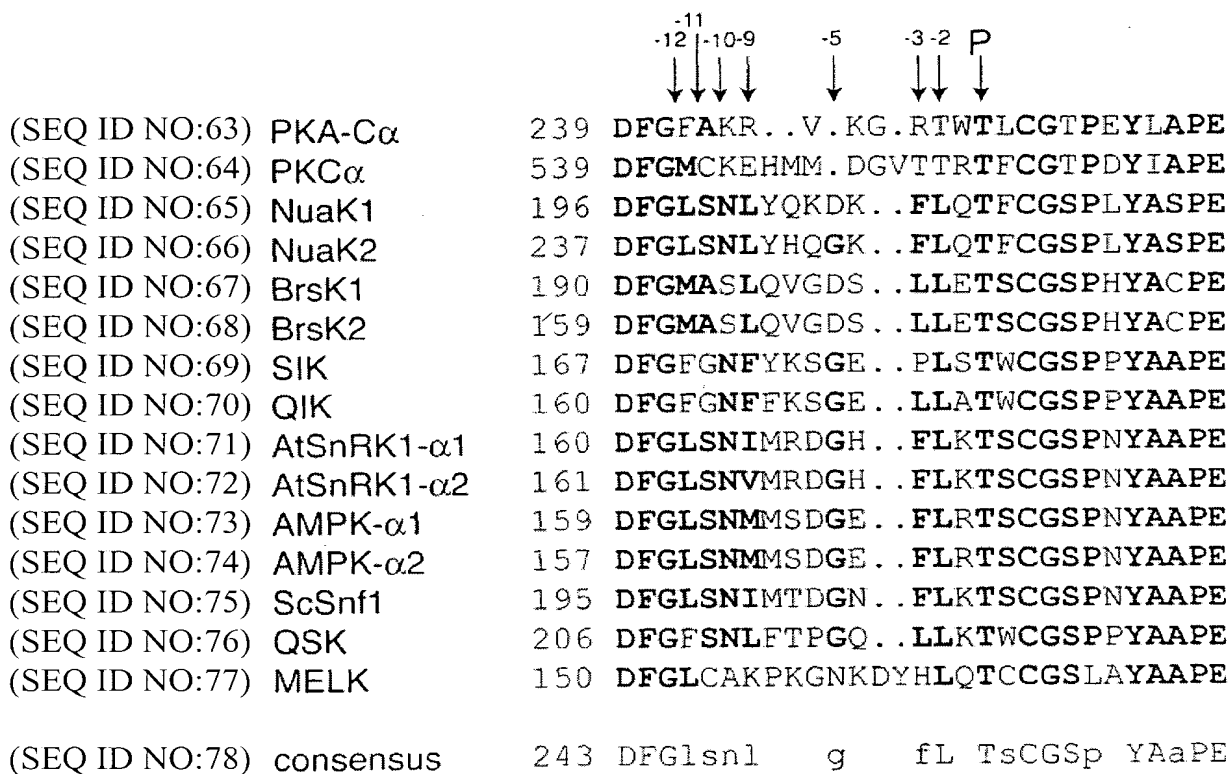
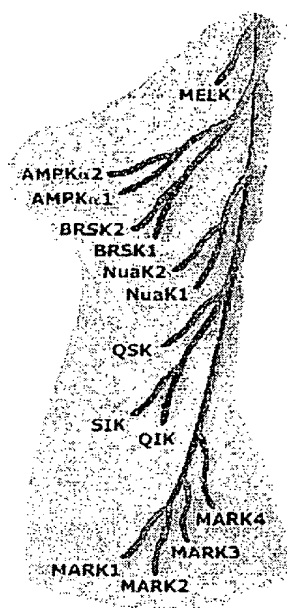


Figure 21A



(SEQ ID NO:73)	AMPK1	159-	DFGLSNMMSDGE--FLRTS	CGSPNYAAPE
(SEQ ID NO:74)	AMPK2	157-	DFGLSNMMSDGE--FLRTS	CGSPNYAAPE
(SEQ ID NO:67)	BRSK1	174-	DFGMASLQVGDS--LLETSC	CGSPHYACPE
(SEQ ID NO:68)	BRSK2	159-	DFGMASLQVGDS--LLETSC	CGSPHYACPE
(SEQ ID NO:65)	NUAK1	196-	DFGLSNLYQKDK--FLQTE	CGSPLYASPE
(SEQ ID NO:66)	NUAK2	193-	DFGLSNLYHQGK--FLQTE	CGSPLYASPE
(SEQ ID NO:69)	SIK	167-	DFGFGNFFYKSGE--PLST	CGSPPYAAPE
(SEQ ID NO:70)	QIK	160-	DFGFGNFFYKSGE--LLATW	CGSPPYAAPE
(SEQ ID NO:76)	QSK	206-	DFGFSNLTIPGQ--LLKTW	CGSPPYAAPE
(SEQ ID NO:79)	MARK1	200-	DFGFSNEETVGN--KLDTE	CGSPPYAAPE
(SEQ ID NO:80)	MARK2	160-	DFGFSNEETVGN--KLDTE	CGSPPYAAPE
(SEQ ID NO:81)	MARK3	196-	DFGFSNEETVCG--KLDTE	CGSPPYAAPE
(SEQ ID NO:82)	MARK4	198-	DFGFSNEETLGS--KLDTE	CGSPPYAAPE
(SEQ ID NO:77)	MELK	150-	DFGLCAKPKGKNDYHLOT	CGSLAYAAPE



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Figure 21B

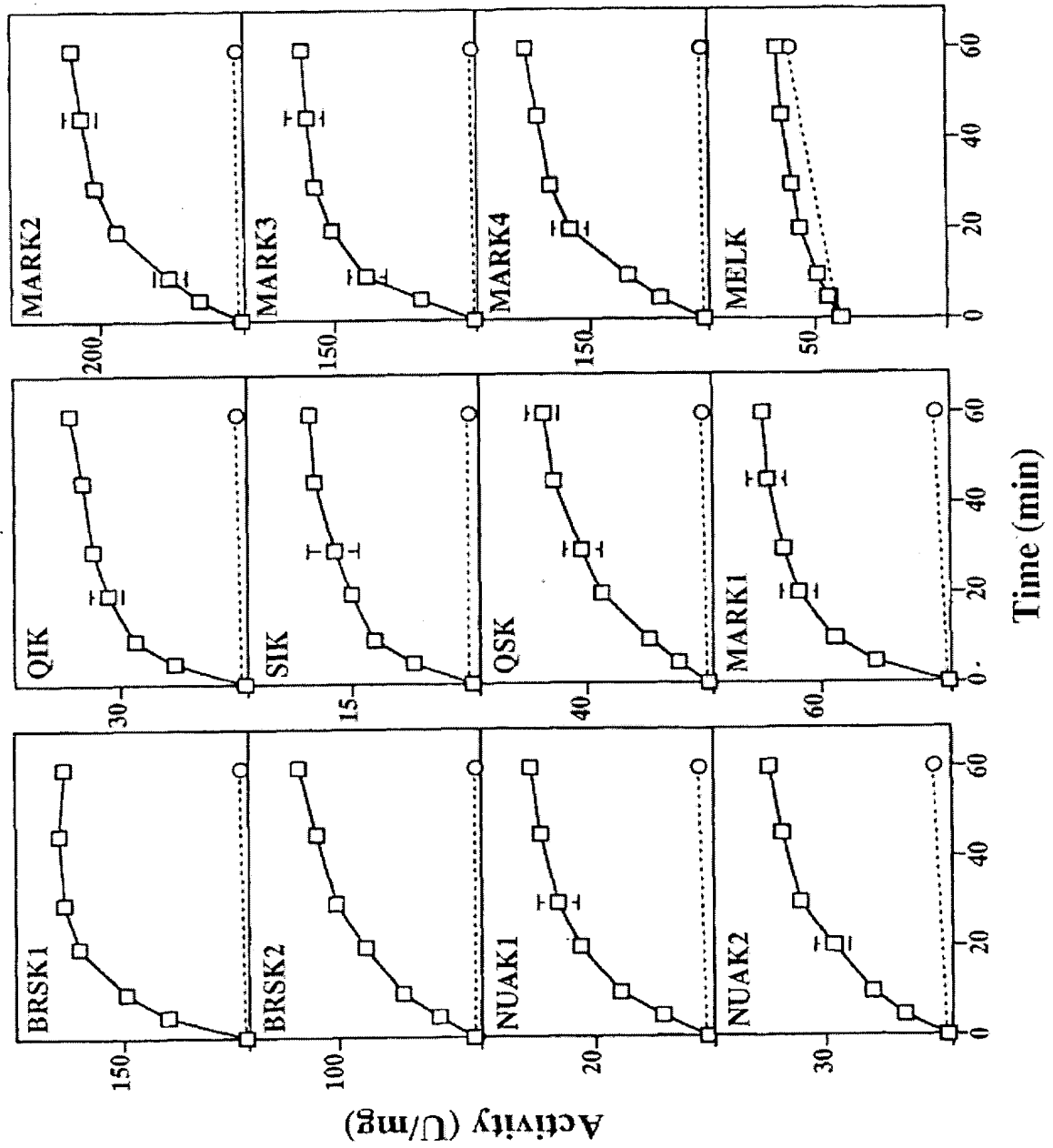


Figure 26A

Peptide				K <sub>m</sub> (mM)	V <sub>max</sub> (U/mg)	V <sub>max</sub> /K <sub>m</sub>
NUAK2	LSNLYHQGKFLQTFCGSPLYRRR	(SEQ ID NO:83)				
SIK	FGNFYKSGEPLSTWCGSPPYRRR	(SEQ ID NO:84)		0.15 ± 0.02	86.8 ± 3.4	578
AMPK	LSNMMSDGEFLRTSCGSPNYRRR	(SEQ ID NO:85)		0.46 ± 0.05	63.9 ± 2.2	139
BRSK2	MASLQVGDSLLETSCGSPHYRRR	(SEQ ID NO:86)		1.40 ± 0.24	94.1 ± 8.3	67
MARK3	MASLQVGDSLLETSCGSPHYRRR	(SEQ ID NO:87)		0.40 ± 0.06	10.6 ± 0.6	26
MELK	FSNEFTVGGKLDFTFCGSPPYRRR	(SEQ ID NO:88)		0.62 ± 0.06	10.2 ± 0.4	16
	AKPKGNDYHLQTCGSLAYRRR	(SEQ ID NO:88)		>3	>60	

Figure 26B

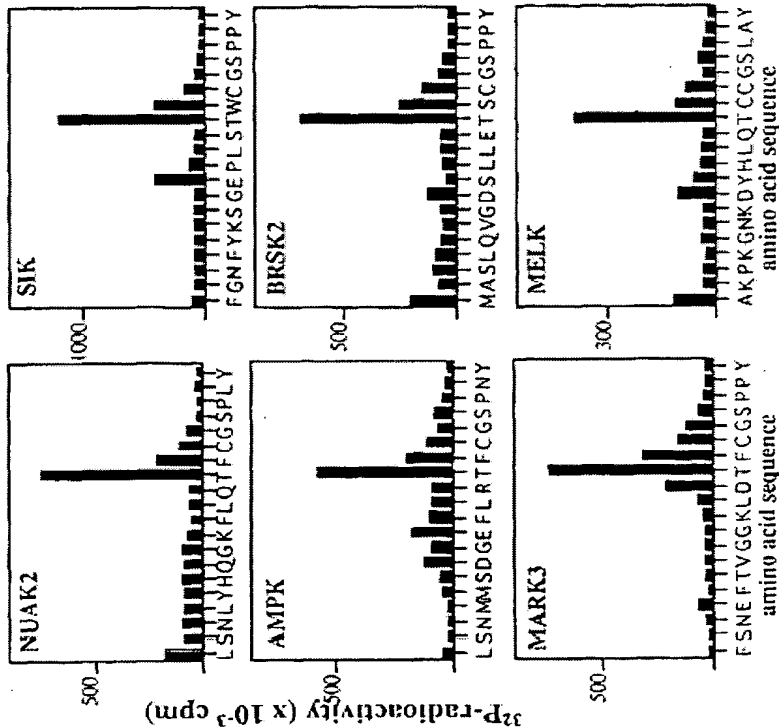
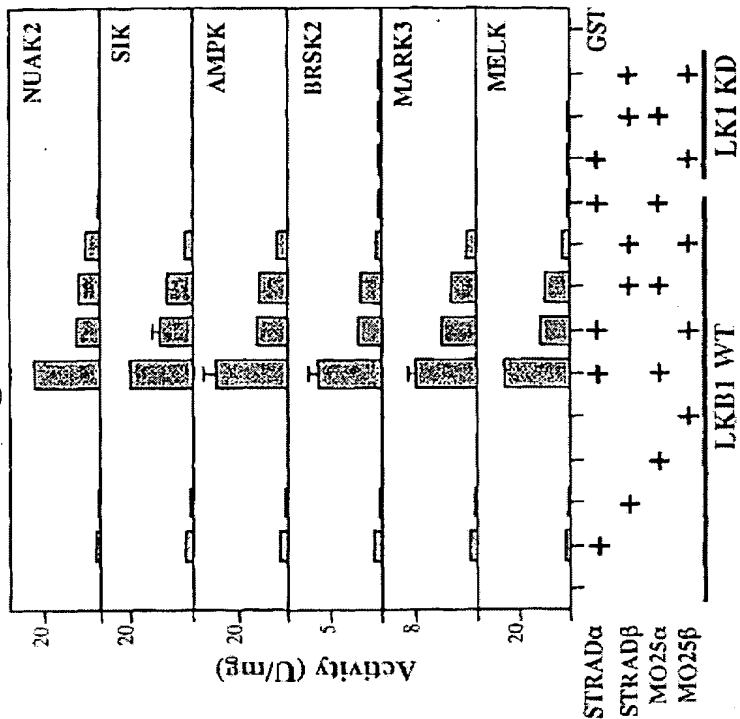
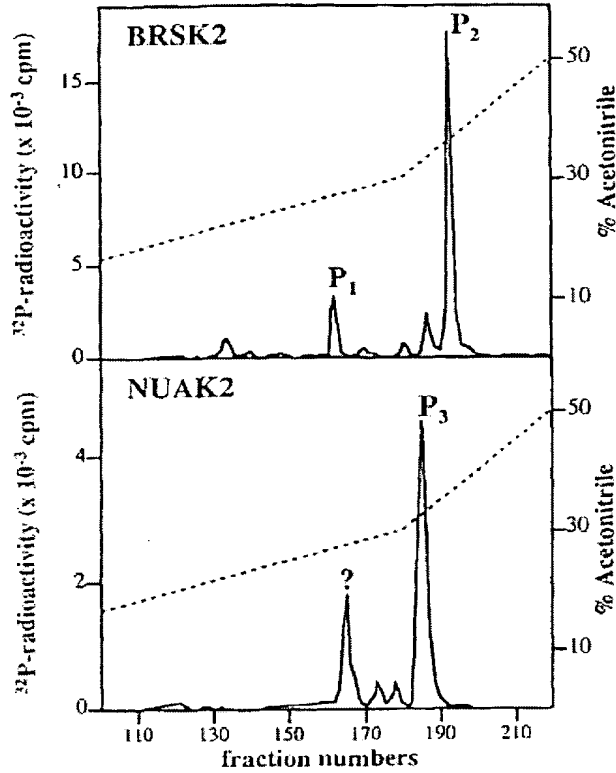
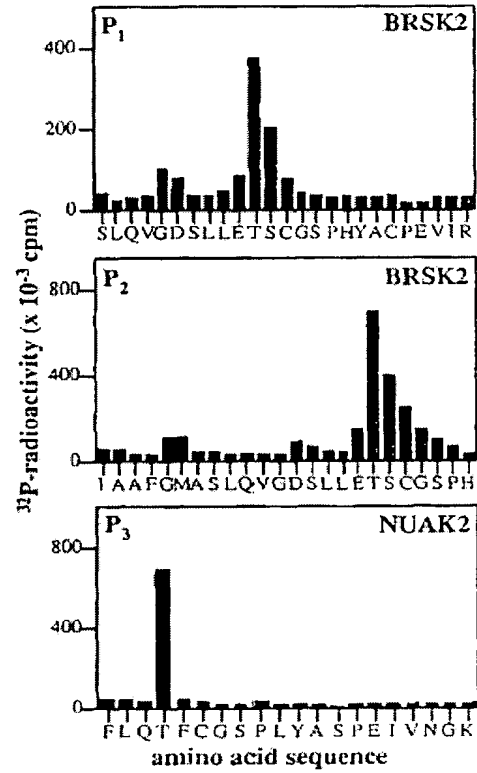


Figure 26C



**Figure 30A****Figure 30B****Figure 30C**

Kinase	Posphopeptide	Mass observed	Theoretical mass
BRSK2 $\text{P}_1$	IAAFGmASLQVGDSLLET(p)SCGSPHYACPEVIR (SEQ ID NO:89)	3268.7870	3628.6680
BRSK2 $\text{P}_2$	SLQVGDSLLET(p)SCGSPHYACPEVIR (SEQ ID NO:90)	2951.4530	2951.3472
NUAK2 $\text{P}_3$	FLQT(p)FCGSPLYASPEIVNGK (SEQ ID NO:91)	2356.1088	2356.1333
MARK4	LDT(p)FCGSPPYAAPELFQGK (SEQ ID NO:92)	2225.9983	2226.1497
MELK	GNKDYHLQT(p)CCGSLAYAAPELIQCK (SEQ ID NO:93)	2970.4421	2970.3648